



Does Not Comply
Corrected Diskette Needed

OIPE

RAW SEQUENCE LISTING

DATE: 04/01/2002

PATENT APPLICATION: US/09/995,804A

TIME: 15:09:53

Input Set : A:\Sequence.lst

Output Set: N:\CRF3\04012002\I995804A.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Engler, Jeffrey A
7 Lee, Jae Hwy
8 Collawan, James F
9 Moore, Bryan A

11 (ii) TITLE OF INVENTION: Receptor-Mediated Uptake of Peptides
12 that Bind the Human Transferrin Receptor

14 (iii) NUMBER OF SEQUENCES: 13

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: Hendricks and Assoc.
18 (B) STREET: P.O. Box 2509
19 (C) CITY: Fairfax
20 (D) STATE: VA
21 (E) COUNTRY: U.S.A
22 (F) ZIP: 22031

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/995,804A
C--> 32 (B) FILING DATE: 29-Nov-2001
33 (C) CLASSIFICATION:

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Hendricks, Glenna M
37 (B) REGISTRATION NUMBER: 32,535
38 (C) REFERENCE/DOCKET NUMBER: engler1

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: 703/425-8405
42 (B) TELEFAX: 703/425-8406

ERRORED SEQUENCES

129 (2) INFORMATION FOR SEQ ID NO: 5:

131 (i) SEQUENCE CHARACTERISTICS:

132 (A) LENGTH: 18 base pairs
133 (B) TYPE: nucleic acid
134 (C) STRANDEDNESS: single
135 (D) TOPOLOGY: unknown

137 (ii) MOLECULE TYPE: DNA (genomic)

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139      (iii) HYPOTHETICAL: NO
141      (iv) ANTI-SENSE: NO
145      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
E--> 147 TGGGATTTTG CTAAAAAC
W--> 148 18 wrapped text
150      (2) INFORMATION FOR SEQ ID NO: 6:
152          (i) SEQUENCE CHARACTERISTICS:
153              (A) LENGTH: 22 base pairs
154              (B) TYPE: nucleic acid
155              (C) STRANDEDNESS: single
156              (D) TOPOLOGY: unknown
158          (ii) MOLECULE TYPE: DNA (genomic)
160          (iii) HYPOTHETICAL: NO
162          (iv) ANTI-SENSE: NO
166          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
E--> 168 GPATGGGATT TTGCTAAACA AC
W--> 169 22
171      (2) INFORMATION FOR SEQ ID NO: 7:
173          (i) SEQUENCE CHARACTERISTICS:
174              (A) LENGTH: 28 base pairs
175              (B) TYPE: nucleic acid
176              (C) STRANDEDNESS: single
177              (D) TOPOLOGY: unknown
179          (ii) MOLECULE TYPE: DNA (genomic)
181          (iii) HYPOTHETICAL: NO
183          (iv) ANTI-SENSE: NO
187          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
E--> 189 TCTAGATCTG ATGAGTAAAG GAGAAGAA
W--> 190 28
192      (2) INFORMATION FOR SEQ ID NO: 8:
194          (i) SEQUENCE CHARACTERISTICS:
195              (A) LENGTH: 54 base pairs
196              (B) TYPE: nucleic acid
197              (C) STRANDEDNESS: single
198              (D) TOPOLOGY: unknown
200          (ii) MOLECULE TYPE: DNA (genomic)
202          (iii) HYPOTHETICAL: NO
204          (iv) ANTI-SENSE: NO
208          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
E--> 210 TTAAGGCTT TAATGGCGCG GATAGATCGC ATGTTTGTAG AGCTCATCCA TGCC
W--> 211 54
213      (2) INFORMATION FOR SEQ ID NO: 9:
215          (i) SEQUENCE CHARACTERISTICS:
216              (A) LENGTH: 68 base pairs
217              (B) TYPE: nucleic acid
218              (C) STRANDEDNESS: single
219              (D) TOPOLOGY: unknown
221          (ii) MOLECULE TYPE: DNA (genomic)
223          (iii) HYPOTHETICAL: NO

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225      (iv) ANTI-SENSE: NO
229      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
E--> 231 TAAAGCTTTT ACGGCCACAC CGGGCTCCAC ATCGGCGGGC GGTGGGTTTT GTAGAGCTCA
W--> 232      60
E--> 234 TCCATGCC
W--> 235      68
237 (2) INFORMATION FOR SEQ ID NO: 10:
239      (i) SEQUENCE CHARACTERISTICS:
240          (A) LENGTH: 29 base pairs
241          (B) TYPE: nucleic acid
242          (C) STRANDEDNESS: single
243          (D) TOPOLOGY: unknown
245      (ii) MOLECULE TYPE: DNA (genomic)
247      (iii) HYPOTHETICAL: NO
249      (iv) ANTI-SENSE: NO
253      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
E--> 255 GATCCCATGC GATCTATCCG CGCCATTAA
W--> 256      29
258 (2) INFORMATION FOR SEQ ID NO: 11:
260      (i) SEQUENCE CHARACTERISTICS:
261          (A) LENGTH: 29 base pairs
262          (B) TYPE: nucleic acid
263          (C) STRANDEDNESS: single
264          (D) TOPOLOGY: unknown
266      (ii) MOLECULE TYPE: DNA (genomic)
268      (iii) HYPOTHETICAL: NO
270      (iv) ANTI-SENSE: YES
274      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
E--> 276 GATCTTAATG GCGCGGATAG ATCGCATGG
W--> 277      29
279 (2) INFORMATION FOR SEQ ID NO: 12:
281      (i) SEQUENCE CHARACTERISTICS:
282          (A) LENGTH: 44 base pairs
283          (B) TYPE: nucleic acid
284          (C) STRANDEDNESS: single
285          (D) TOPOLOGY: unknown
287      (ii) MOLECULE TYPE: DNA (genomic)
289      (iii) HYPOTHETICAL: NO
291      (iv) ANTI-SENSE: NO
295      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
E--> 297 GATCCACCCA CCGCCGCGG ATGTGGAGCC CGGTGTGGCC GTAA
W--> 298      44
300 (2) INFORMATION FOR SEQ ID NO: 13:
302      (i) SEQUENCE CHARACTERISTICS:
303          (A) LENGTH: 44 base pairs
304          (B) TYPE: nucleic acid
305          (C) STRANDEDNESS: single
306          (D) TOPOLOGY: unknown
308      (ii) MOLECULE TYPE: DNA (genomic)

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310 (iii) HYPOTHETICAL: NO

312 (iv) ANTI-SENSE: YES

316 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

E--> 318 GATCTTACGG CCACACCGGG CTCCACATCG GCGGGCGGTG GGTG

W--> 319 44

VERIFICATION SUMMARY

DATE: 04/01/2002

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TIME: 15:09:54

Input Set : A:\Sequence.lst

Output Set: N:\CRF3\04012002\I995804A.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:147 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:5
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:168 M:254 E: No. of Bases conflict, Input:0 Counted:22 SEQ:6
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:189 M:254 E: No. of Bases conflict, Input:0 Counted:28 SEQ:7
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:210 M:254 E: No. of Bases conflict, Input:0 Counted:54 SEQ:8
L:211 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:231 M:254 E: No. of Bases conflict, Input:0 Counted:60 SEQ:9
L:232 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
M:254 Repeated in SeqNo=9
L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:255 M:254 E: No. of Bases conflict, Input:0 Counted:29 SEQ:10
L:256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:276 M:254 E: No. of Bases conflict, Input:0 Counted:29 SEQ:11
L:277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:297 M:254 E: No. of Bases conflict, Input:0 Counted:44 SEQ:12
L:298 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:318 M:254 E: No. of Bases conflict, Input:0 Counted:44 SEQ:13
L:319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13